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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=16; hr=16; min=4; sec=15; ms=408;]

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Reviewer Comments:

<210> 11

<211> 26

<212> PRT

<213> Beta vulgaris

<400> 11

His Asp Gln His Arg Asp Met Arg Leu Asp Ile Asp Asn Met Ser Tyr Glu
1 5 10 15

Glu Leu Leu Ala Leu Glu Glu Arg Ile Gly
20 25

The amino acid numbers "20" and "25" are misaligned, above. The "20" should be under the second "Leu" and the "25" should be under "Arg." Also, although the above <211> response is "26," 27 amino acids are shown.

Application No: 10552686 Version No: 2.0

Input Set:

Output Set:

Started: 2008-06-13 14:01:54.273
Finished: 2008-06-13 14:01:54.826
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 553 ms
Total Warnings: 0
Total Errors: 5
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

Error code	Error Description
E 323	Invalid/missing amino acid numbering SEQID (11)at Protein (20)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (21)
E 323	Invalid/missing amino acid numbering SEQID (11)at Protein (25)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (26)
E 331	Count of Protein differs from the <211> tag Input: 26

SEQUENCE LISTING

<110> CropDesign N.V.

<120> Stress Tolerance

<130> 4982-12

<140> 10552686

<141> 2005-11-21

<150> PCT/EP04/50513

<151> 2004-04-13

<150> EP 03076064.9

<151> 2003-04-11

<160> 11

<170> PatentIn version 3.2

<210> 1

<211> 1344

<212> DNA

<213> Beta vulgaris

<220>

<221> misc_feature

<222> (3)..(3)

<223> n is a, c, g, or t

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caactacgaa ttcattgatca gatcataatg cttgattctg caaaagcaac gacagagaca	540
gttgctgcat tgagatctgg tgctagtgtc atgaaggcta tgcagaaagc aacaaacatt	600
gatgatgttg acaagacaat ggatgagatc aatgagcaga ccgataactt gagacagata	660
caggaggcac tagctactcc tgttggtgca actgattttg atgaggatga attggaagct	720
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<210> 2
<211> 224
<212> PRT
<213> Beta vulgaris

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          20          25          30

Thr Leu Glu Met Leu Glu Lys Lys Glu Gln Leu Leu Met Lys Lys Ala
          35          40          45

Thr Ala Glu Val Glu Lys Ala Lys Glu Phe Thr Arg Ala Lys Asn Lys
          50          55          60

Arg Ala Ala Ile Gln Cys Leu Lys Arg Lys Arg Leu Tyr Glu Gln Gln
65          70          75          80

Val Glu Gln Val Gly Asn Phe Gln Leu Arg Ile His Asp Gln Ile Ile
          85          90          95

Met Leu Asp Ser Ala Lys Ala Thr Thr Glu Thr Val Ala Ala Leu Arg
          100          105          110

Ser Gly Ala Ser Ala Met Lys Ala Met Gln Lys Ala Thr Asn Ile Asp
          115          120          125

Asp Val Asp Lys Thr Met Asp Glu Ile Asn Glu Gln Thr Asp Asn Leu
          130          135          140

Arg Gln Ile Gln Glu Ala Leu Ala Thr Pro Val Gly Ala Thr Asp Phe
145          150          155          160

Asp Glu Asp Glu Leu Glu Ala Glu Leu Glu Glu Leu Glu Gly Ala Glu
          165          170          175

Leu Glu Glu Gln Leu Leu Gln Pro Phe Thr Thr Ala Pro Thr Ala Pro
          180          185          190

Ile His Val Pro Glu Gly Lys Leu Pro Ala Arg Pro Thr Pro Gln Lys
          195          200          205

Asn Ser Glu Glu Asp Glu Leu Ala Ala Leu Gln Ala Glu Met Ala Leu
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<210> 3
<211> 1341
<212> DNA
<213> Beta vulgaris

<220>
<221> misc_feature
<222> (934)..(934)

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<223> n is a, c, g, or t

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tcgagttaac ctaatcactc cattcttatt tcctctcgga aaaaaaccta atcaatcaac    240
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cccaatcacg gatatttggt aataaaatgt gctgtgtagg ttgctgatg ttgttgatta   1140
ggcgtagtt ctccttggtc caggtcttga ttgcacctta ttctcgatgt aaatttcaga   1200
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<210> 4

<211> 154

<212> PRT

<213> Beta vulgaris

<400> 4

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          20           25           30

Lys Glu Gln Val Leu Leu Lys Lys Ala Gly Ala Glu Val Glu Lys Ala
          35           40           45

Lys Glu Phe Thr Arg Ala Lys Asn Lys Arg Ala Ala Ile Thr Cys Leu
          50           55           60

Lys Arg Lys Arg Leu Tyr Glu Gln Gln Ile Glu Gln Leu Gly Asn Met
65           70           75           80

Gln Leu Arg Ile His Asp Gln Met Ile Leu Leu Glu Gly Ala Lys Ala
          85           90           95

Thr Thr Glu Thr Val Asp Ala Leu Arg Ser Gly Ala Ser Ala Met Lys
          100          105          110

Ala Met Gln Lys Ala Thr Asn Ile Asp Asn Val Asp Lys Thr Met Asp
          115          120          125
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 130 135 140

Ser Ala Pro Ile Gly Ala Ala Ala Asp Phe
 145 150

<210> 5
 <211> 1019
 <212> DNA
 <213> Beta vulgaris

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> n is a, c, g, or t

<220>
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 <222> (1001)..(1001)
 <223> n is a, c, g, or t

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 cgtcaatctc gtaagtgcga gaaagaagaa aaagctgaga aactcaaagt caagaaagca 180
 atcgagaaaag gaaacatgga tggagctcga atttacgccg aaaacgcaat tcgtaagcgt 240
 actgaacaga tgaactactt gcgcctcgct tctgcgctcg acgccgtcgt ttcgcgcctc 300
 gatactcaag ctaagatgca aaccatcgga aaatcgatgg gatcaattgt taaatcgctt 360
 gagtcgtctt tgaataccgg taatttgcag aagatgtcgg agacaatgga caattttgag 420
 aagcaatttg ttaatatgga agttcaggct gagtttatgg agagttctat ggctgggagt 480
 acttcgcttt cgactcccga aaccgagggt aatagtttga tgcagcagggt ggcggatgat 540
 tatggccttg aggtttctgt gggtttgctt caggetgctg gacatgctat tcctgttccg 600
 aaggcggcgg agaagggtga tgaggatgat cttaccagga ggctcgccga gctcaaggct 660
 cgagggtgaa gtcaaaggta aaaagggttaa ggttttattg ataatgttgt atagattatg 720
 agctttactg atgatcaacc ctctgtgata tgggggtttg atgataattt gctctatatt 780
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<210> 6
 <211> 204
 <212> PRT
 <213> Beta vulgaris

<400> 6
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 20 25 30

Lys Ala Glu Lys Leu Lys Val Lys Lys Ala Ile Glu Lys Gly Asn Met
 35 40 45

Asp Gly Ala Arg Ile Tyr Ala Glu Asn Ala Ile Arg Lys Arg Thr Glu

50	55	60
Gln Met Asn Tyr Leu Arg Leu Ala Ser Arg Leu Asp Ala Val Val Ser		
65	70	75 80
Arg Leu Asp Thr Gln Ala Lys Met Gln Thr Ile Gly Lys Ser Met Gly		
	85	90 95
Ser Ile Val Lys Ser Leu Glu Ser Ser Leu Asn Thr Gly Asn Leu Gln		
	100	105 110
Lys Met Ser Glu Thr Met Asp Asn Phe Glu Lys Gln Phe Val Asn Met		
	115	120 125
Glu Val Gln Ala Glu Phe Met Glu Ser Ser Met Ala Gly Ser Thr Ser		
	130	135 140
Leu Ser Thr Pro Glu Thr Glu Val Asn Ser Leu Met Gln Gln Val Ala		
145	150	155 160
Asp Asp Tyr Gly Leu Glu Val Ser Val Gly Leu Pro Gln Ala Ala Gly		
	165	170 175
His Ala Ile Pro Val Pro Lys Ala Ala Glu Lys Val Asp Glu Asp Asp		
	180	185 190
Leu Thr Arg Arg Leu Ala Glu Leu Lys Ala Arg Gly		
	195	200

<210> 7
 <211> 1510
 <212> DNA
 <213> Beta vulgaris

<220>
 <221> misc_feature
 <222> (2)..(3)
 <223> n is a, c, g, or t

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ccagtagccg agaaaccagc tgagaagcca gctgagaagg cagttctacc acctgaagct	180
gagaaactag ctgcagctga atcagctgaa gccgagaagc cagctgattc agccgaggct	240
aagatagctc aacaagtctc attcaaagag gagactaatg ttgcaagtga gctacctgag	300
ctacatagaa aggctctcga ggacttgaag aaacttattc aagaagccct cgagaagcac	360
gagttctctt ctctctctcc tccgcctccg cctgctccag ctaaagttga ggagaaggcg	420
gaagagaaga aagaggaaca acctccatcc accacctcca ccaccaccac caccaccacc	480
gcggtttcag atgaggttgc tgttgctcct ccatccgaag aggccccgaa aactgacgag	540
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ggtgaggata ttaaagaaac tatagtagtc gaggttgcca caactacagc agcaccagta	720
ctaacagaac cagaatctgt tgaggagaca caaaagaag ctgaagttgt agtggaagaa	780
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agtgatgtaa ttctattgaa attcttaaga gcaagagatt atagagtga agatgcttct	900
actatgatta gaaatactgc tcggttgaga aaagaatttg aggttgattc ttacttgat	960
gaagatcttg gaaatgatta tgagaaagtt gtttttacac atggagttga taaacaaggt	1020

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cgctctgttt gttataatgt gtttggagag tttcaaaata aggaacttta tcagaatact 1080
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<210> 8
<211> 427
<212> PRT
<213> Beta vulgaris

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          20          25          30

Leu Pro Pro Glu Ala Glu Lys Leu Ala Ala Ala Glu Ser Ala Glu Ala
          35          40          45

Glu Lys Pro Ala Asp Ser Ala Glu Ala Lys Ile Ala Gln Gln Val Ser
          50          55          60

Phe Lys Glu Glu Thr Asn Val Ala Ser Glu Leu Pro Glu Leu His Arg
65          70          75          80

Lys Ala Leu Glu Asp Leu Lys Lys Leu Ile Gln Glu Ala Leu Glu Lys
          85          90          95

His Glu Phe Ser Ser Pro Pro Pro Pro Pro Pro Pro Ala Pro Ala Lys
          100          105          110

Val Glu Glu Lys Ala Glu Glu Lys Lys Glu Glu Gln Pro Pro Ser Thr
          115          120          125

Thr Ser Thr Thr Thr Thr Thr Thr Thr Ala Val Ser Asp Glu Val Ala
          130          135          140

Val Ala Pro Pro Ser Glu Glu Ala Pro Lys Thr Asp Glu Ala Ser Pro
145          150          155          160

Lys Val Glu Glu Glu Pro Ala Lys Ile Val Glu Gln Pro Pro Thr Thr
          165          170          175

Pro Ala Glu Glu Pro Glu Pro Ala Lys Thr Pro Glu Val Val Val Ala
          180          185          190

Glu Glu Glu Lys Thr Gly Glu Asp Ile Lys Glu Thr Ile Val Val Glu
          195          200          205

Val Ala Thr Thr Thr Ala Ala Pro Val Leu Thr Glu Pro Glu Ser Val

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210	215	220
Glu Glu Thr Pro Lys	Glu Ala Glu Val Val	Glu Glu Ser Pro Lys
225	230	235 240
Glu Pro Glu Glu Val	Ser Ile Trp Gly Ile	Pro Leu Leu Ala Asp Glu
245	250	255
Arg Ser Asp Val Ile	Leu Leu Lys Phe Leu	Arg Ala Arg Asp Tyr Arg
260	265	270
Val Lys Asp Ala Phe	Thr Met Ile Arg Asn	Thr Ala Arg Trp Arg Lys
275	280	285
Glu Phe Glu Val Asp	Ser Leu Leu Asp Glu	Asp Leu Gly Asn Asp Tyr
290	295	300
Glu Lys Val Val Phe	Thr His Gly Val Asp	Lys Gln Gly Arg Pro Val
305	310	315 320
Cys Tyr Asn Val Phe	Gly Glu Phe Gln Asn	Lys Glu Leu Tyr Gln Asn
325	330	335
Thr Phe Ser Asp Ala	Glu Lys Arg Lys Lys	Phe Leu Arg Trp Leu Ile
340	345	350
Gln Phe Leu Glu Lys	Thr Ile Arg Thr Leu	Asp Phe Ser Pro Glu Gly
355	360	365
Ile Asn Ser Phe Val	Leu Val Asn Asp Leu	Lys Asn Ser Pro Gly Tyr
370	375	380
Gly Lys Arg Asp Leu	Tyr Lys Val Ile Asp	Lys Phe Leu Glu Ile Leu
385	390	395 400
Gln Asp Asn Tyr Pro	Glu Phe Ala Ala Lys	Gln Leu Cys Ile Asn Val
405	410	415
Ser Trp Trp Ser Trp	His Thr Thr Gly Ser	Ile
420	425	

<210> 9
 <211> 2052
 <212> DNA
 <213> Beta vulgaris

<220>
 <221> misc_feature
 <222> (2049)..(2049)
 <223> n is a, c, g, or t

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	ggatgaatat tccaatagaa aatcttcttg tcttgctatc tccaggagag ggcctagcct	180
	tgttttaagg gactcagcgg agaacaacaa agatcggaat gttcagggtt gcagccgagt	240
	tggatgtggc agcaagttga attcagtga ggtatgctaaa gttagctctc cgagtaaaagt	300

caaatctcca	aaaactcctt	tccgttcata	tgctcaagga	aaagaaacca	ttggaagttc	360
atccagaact	ctggcttctc	ctagtccttt	taaaaaatct	ctttcagacc	ggaagaaaaa	420
actgccttct	aatcttgaca	ctgattcaga	aatgtgcagt	cttcaagatg	aatccgagga	480
agtctctgga	aagacccgga	taaggggttca	gcccgaacca	gaagatcatg	attccattga	540
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aaatactcag	aggtttgggt	tggggcgcca	agattctgct	gcaagttctg	cttcattttc	660
tttaaataaa	accaaccaag	ggcaaagaaa	tggtagtggt	ggtggtgcta	gtgctaacag	720
gtataatctg	cgacaattaa	aatgtaactc	aatctctgac	gttggtccat	caggttctcc	780
gcagtctgct	gaatcaagtc	tcagtaagaa	gagggacaca	ggttgtagga	agagaaatgg	840
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taggaggaat	gactatccaa	atcgtggaat	atcaatatct	gatacaaggc	gtaccagaag	960
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